

## FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCGAGGACTGT  
 GTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG  
 TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAAATCTTACTTTTAGGAGGA  
 CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACCCATGAAGGAGTATGTG  
 CTCCTATTATTCTGCTTTGTGCTCTGCGAAACCCCTTCTTTAGCCCTTTCACACATCGCACT  
 GAAGAATATGATGCTGAAGGATATGGAAGACAGATGATGATGATGATGATGATGATGATGATG  
 ATGATGATGATGAGGACAACTCTCTTTTTTCCAAACAGAGAGCCAAAGGCCAATTTTTTCCA  
 TTTGATCTGTTTTCCAATGTGTCCATTGGATGTTCAGTGCTATTACAGAGTGTGTACATTGCTC  
 AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTGTGATACTCGAATGCTTGATCTTC  
 AAAACAATAAAAATTAAGGAAATCAAAGAAAATGATTTTAAAGGACTCATTCTCATTATGGT  
 CTGATCCTGAACAACAACAAGCTAACGAAGATTCAACCAAAAGCCTTTCTAACCACAAAGAA  
 GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAAATACCCTTAATCTTCCCAAAAT  
 CATTAGCAGAACTCAGAATTCATGAAAATAAAGTTAAGAAAATACAAAGGACACATTTCAAA  
 GGAATGAATGCTTTACACGTTTTGGAAAATGAGTGCAAAACCTCTTGATAATAATGGGATAGA  
 GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGAGAGAAGCAAACTGACCT  
 CAGTTCTTAAAGGCTTACCACCACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA  
 ACAGTGGAACCTTGAGGATTTTAAACGATACAAAGAACTACAAAGCTGGGCCCTAGGAAACAA  
 CAAAATCAGAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT  
 TGGAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACAGAGTTGAAATACCTCCAGATA  
 ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTTCTGTCCAACGTGCC  
 AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG  
 AAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACTTT  
 GGAATGTAAATAATTAGTAATTTGGTAATGTCCATTTAATATAAGATTCAAAATCCCTACATT  
 TGGAACTCTTGAACCTCTATTAATAATGGTAGTATTATATATACAAGCAAATATCTATTCTCA  
 AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAAATTTCAACGGAATTTTGCCAAACTATT  
 GATACATAAAGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCCTTTTTGCGTACAAATGAT  
 CTTACATAAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAGTAAGATATTCCGTA  
 TTTAACACTTTGTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT  
 TAGCAAAATTTGTGCTCTTTCACTTTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT  
 GAAGAGTGCATTACACTATTCTTATTCTTAGTAACCTTGGTAGTACTGTAATATTTTAAAT  
 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCCGT  
 CTTTATGTTTAAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTTCAATACCAACTGTGA  
 TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTATT  
 ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACCTCGCATTTT  
 AATGATCCGCTATTATAAGCTTTTAAATAGCATGAAAATTTGTAGGCTATATAACATTGCCAC  
 TTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGAAGACCTTGCTTGAAGAGCCTGGA  
 CACTAACAAATTTACACCAAAATGTCTCTTCAAATACGTATGGACTGGATAACTCTGAGAAA  
 CATACCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA  
 TATAAATGCTCAGAGTCTTTATGTATTTCTTATTGGCATTCAACATATGTAAATCAGAAA  
 ACAGGGAATTTTCATTAATAAATATTGGTTTGAAT

## FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR  
SHFFPFDLFFMCPFGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL  
TSLYGLILNNNKLTKIHPKAFLTTKKLRRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ  
KDTFGKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD  
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPIRVREIHLENNKLKKIPSGLP  
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNNPVKYWEMQPATFRCVLSRMSV  
QLGNFGM

### Signal sequence.

amino acids 1-15

### N-glycosylation site.

amino acids 281-285

### N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

### Leucine zipper pattern.

amino acids 154-176



## **FIGURE 4**

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE  
TWHFDLQPPFGVMRCVLCACEAPQWGRRTRGPGRVSCCKNIKPECPPTACGQPRQLPGHCCQT  
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAEEERARGDGHTDFVALLTGPRSQAVAR  
ARVSLLRSSSRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL  
LRAEQLHVALVTLTHPSGEVWGPIIRHRALAAETFSAILTLLEGPPQQGVGGITLLTLSDTED  
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLPNLTVQEMD  
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN  
GSLIYQVQVVGTSSEVVAMTLETKPQRRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHL  
LQNELFLNVGTKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVVKSAAGHAWLS  
LDTHCHLHYEVLLAGLGGSEQGTVAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR  
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLREAAAGGVRLGAPDTASAAPPVV  
PGLPALAPAKPGGPGRPDPNTCFEFGQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP  
PPSCPHPVQAPDQCCPVCPEKQDVRDLPLPRSRDPGEGCYFDGDRSWRAAGTRWHHPVVPF  
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVRNPTDCKQCPVSGAHPLGDPMQADG  
PRGCRFAGQWFPESQSWHPSPVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCSGSGKESRCCS  
RCTAHRPPETRTDPELEKEAEGS

**Signal sequence.**

amino acids 1-23

**N-glycosylation sites.**

amino acids 217-221, 351-355, 365-369, 434-438

**Tyrosine kinase phosphorylation sites.**

amino acids 145-153, 778-786

**N-myristoylation sites.**

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,  
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,  
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,  
905-911

**Amidation site.**

amino acids 87-91

**Cell attachment sequence.**

amino acids 165-168

**Leucine zipper pattern.**

amino acids 315-337

[illegible]

GGGAGCAGCCCTTAGCCGCCACCCTCGCTCTCGCAGCTCTGTGCCCACGTGCCACGCCGCGCCCGTCACTGCG  
TCTCGTCTCCGGCTCCCGCGCCCTCCGCGCGCGC**ATG**CAGCCCGCCGCGCGCCCTCCAGGCGCCGGGTCCGCGAGTCCG  
TGCCCGCGCTGGCCCTGTGCTGTGCTGTCTGGAGCGGGCGCCGAGCGCTCTCGCAGCAACCGCGTCCGCG  
CGCGCGCCCTTGTTGTGCGCCCGCGCGCTCGCGCGCGCAGCCCTCGCCGAATGGGGGTGTGTGTCACCTCGCGCCCTTG  
AGCCGACCGCCGACGACCCGCGCCCGCGCGCGAGCTTGCTACAGTGCACCTGCCCCGGGAATCTCCGCG  
CCAACCTGCCAGCTTGTGTGCAGATCTTGTGTCAGCAACCCCTTGTACCATTGCACTGCAGCAGCAGCAGCAGCA  
CGACGACGAGTGGTCACTCTGCAATTTGCAATGAAGGCTATGAAGGTTCCCACTGTGAACAGCACTCTCCAGCTT  
TCCCGACGACTGGCTGGACCGCAATCCATGCGACCCAGACGCTTACGCTGTCTCTGCTCAGGACGCTTGA  
AAATCTCGCTCGCTCTCGAGCAGCGGTGACATCGCTTCTCGCGCAGCGCAAAACAGGAGCAAAAGTTGTAGAAA  
TGAAATGGGATCAAGTGGAGTGATCCGAGATATGCTGCTGTGGAAATGGCAATCTTAACAGCTCTCGCGGTGGCC  
GCTCTGTATCTCTTTGAAGTGGCCAGAACACTCTCAGTCAAGATTCCGCAAGATGCCACTGCCTCTACTGATTTTGC  
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGTCTCTCATAGATGACGAGCAAGTGACCCCTCTACGGCTT  
CAGGGGACCTGGCTCTCTGGAGGAGATGCTGCGCTTGGGAATAATCACTTATTGGTTTGTGAATGATCTGTG  
TGACTTAAGTCTATTTGGCTTTTGGCTTAATCTGGTGTGGAAGTGCAGCCATGTGCTGCGCGGGGAGAGTACG  
CAAAATGACTGGAGTGTTCAGAAAAGGAAATGACACCAAGGCGCTCAGGACCACTTCTCTGTACTGTGTGT  
AGGAGCAGTACGTGGGTACTTCTGTGAAGAATAACGATCTGTCCGAGAGGAAACCTTGCACAAAACAGCGAGCT  
GTATTGTGCAAAATGAAAGCAAGATGGGAGCAATTTCACTCTTGTGCTTCTGGTTATACCTGGAGAGCTT  
GCCAGTCCAAGATTGACTAGCTCTAGACCAATGAGAAATGAGACAATGCAATCTTCCAGTCTCAGTGGAT  
TCAACTGCCAGTGTCCAGAGATGATCTCGGATCTGCTTGTGAAGAAAGTGGACACCTTCGCGCTCTGCTTCGCT  
CGCAGAAACACGGCAGCTGATATGTGACGGGGTACACTTTACTCGAATCGAGCCGGGCTTCAGCGGCCG  
CAATGTGCCAGCTTATPACTCTGTGCGCTCAGCCCTGTGCTCATGCGACCTGCGCAGCGGTGGCAGCACAGCT  
ACAAATGCTCTGTGATCCAGTTACCAATGGCTCTACTGTGAGGAGAAATATGATGATGCTCTCCGCTCCAT  
GCTCTGAATGCAGCCACCTCGAGGGACCTCGTTTAATGGCTATGAGTGTGTGCTCGGCAGAAATACAAAGGAACAC  
ACTGTGAATTTGACAAAGCTCTTGCTGCTTAACGTCAGCTGTGTGACAGGACGCCACTGTGACAGCAGCGCCCTGA  
ATGGCAGCTGCATCTGTGACCCCGGTTTACAGTGAAGATGCGCAATGCATATGCAATGAATGATGACAGTAACT  
CTGTCGCCACCTGTTGGGAGCTGCTCGACCAAGCCCAATGGTTATACATGCGCACTGCCCGCATGGTTGTGGGAG  
CAAACTGTGAGATCACTCCAATGGAACTCGGGCAGATGGCGGAGAGCTTCAACAAATGCCACGGCAGCTCCC  
TCTACATCATCATTTGAGCGCTTCTCGTGGCTTCATCCTTATGCTGATCATCCTGATCTGTGGGGATTGGCCGA  
TCAGCCGCATTTGAATACCCAGGTTCTTCAGGCCCGCACTTGAAGGAGTTTCAACATTCGCGCAGCATCGACGGC  
AGTTTCAAGAAATGCCATTGACATCTCCGCTAGCCAGTTTGTGGAAGAAATCCGGCGTCGAATGTATGATGTGA  
GCCCATCGCCTATGAGAGTACAGTCTGATGACAAACCTTGGTCAACACTGATTTAAACATAAAGATTT**GTAA**T  
CTTTTGTGATTAATTTTCAAAGAAATGAGATATGACTACACTTAATTAATTTTGAAGAAAATAAAGAGCT**AA**A  
GAAATTTAAATCTGAGCTGCTCAAGAGTCTTCAAGTAAATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG  
GAAAAAATTTTAAAAACAAAATTTGTGAAACCTATAGACGATGGTTTAATGTACCTCAGCTCTCTAAACTGT  
GTGCTCTACTAGTGTGTGCTTTTCACTGTAGACATATACAGAGCCAGATTAATTTCTGTGGTGTGTACA  
GAATAGCTCTAATCAAGGAGATTTCTGTGTAGCTTGTAGTGCGCGGTTCTGAGTAGAGTTAGGAAAACACG  
GTAACTGATCATATGATGATTAATAGATATACCGGTTATCTAAAAGAGTGTGGAATGTCTGTTTGTGGAAA  
AGAAACTGAGTATTAATTTACTAATCTCTAACCGGAATGAAATAGCCCTTTGCTCTATTCTGTGCATGGGTAACT  
TTATTTCTGCACCTGTTTGTGTAAGTGTGGAAACACTTTCTCGAGTTTGTTTTGTGCTATTTCGTAAACGTCG  
TCGAACTAGGCCCTCAAAACATACGTAAACGAAAGGCCATAGCAGGCGAAATCTGATGATTGTAATCTATATT  
TTCTTTAAAAGAGTCAGGGTCTATATTGTGAGTAAATTAATTTACATTGAGTTGTGTGTGTCGAGAGGTAG  
TAAATGATAAGAGTACGTGTTCTCTCAGTAGGAGTAAATTTCTACATGTCAGCTTATTATTCTCAGAGATGT  
TTTGTGGCTGATTGATTGATATGTGCTTCTCTGTGATCTTGTCTAATTTCCAACCATATTGAATAAATGTGATC  
AGTCA

## FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLLGGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNNGVCTSR  
PEPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNCHHGNCSSSSSSSDGYLCICN  
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV  
VEMKWDQVEVIPDIACGNASSNSAGGRLVSFEVPQNTSVKIRQDATA SLILLWKVTATGFQ  
QCSLIDGRSVTPLQASGGVLVLEMLALGNNHFIFGVNDSVTKSIVALRLTLVVKVSTCVPG  
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTFCCEEYDACQRKPCQNNASCIDANEKQD  
GSNFTCVCLPGYTGELCQSKIDYCILDP CRNGATCISL SGFTQCQCEGYFGSACEEKVDPC  
ASSPCQNNGTCTYDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG  
YHGLYCEEEYNECL SAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDP CANVSC L NGATC  
DSDGLNGTICAPGFTGEECDIDINECD SNPCHHGSCLDQPNGYNCHCPHGWWGANCEIHL  
QWKS GHMAESLTNMPRHSLYIIIGALCVAFILMLIILVIGICRISRIEYQGSRRPAYEEFYN  
CRSIDSEFSNAIASIRHARFGKSRPAMYDVSPIAYEDYSPDDKPLVTLIKTKDL

**Signal sequence.**

amino acids 1-28

**Transmembrane domain.**

amino acids 641-660

**N-glycosylation sites.**

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,  
375-379, 442-446, 549-553, 564-568

**Glycosaminoglycan attachment site.**

amino acids 320-324

**Tyrosine kinase phosphorylation sites.**

amino acids 490-498, 674-682

**N-myristoylation sites.**

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,  
373-379, 449-455, 480-486, 562-568, 565-571

**Amidation site.**

amino acids 702-706

**Aspartic acid and asparagine hydroxylation site.**

amino acids 520-532, 596-608

**EGF-like domain cysteine pattern signatures.**

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,  
491-503, 529-541, 567-579, 605-617

## **FIGURE 7**

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTCAGGC'TTTCAGGGGGACTGGTCCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC  
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC  
TGGTTATACTGGAGAGCTTTGCCAACCGAACCTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGGAG

CCCTTTCAGGC'TTTCAGGGGGACTGGTCCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA

## 090716Z 083001

CTCTGGAAGGTCACGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA  
CCCCCCTTTCAGGCTTTTCAGGGGGACTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATA  
ATCACTTTATTGTTTGTGTAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT  
CTGGTGGTGAAAGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAAATGACTTGGAGTGTTC  
AGGAAAAGGAAAAATGCACCAGAAAGCCGTCAAGAGCAACTTTTTCTGTACTCTGTGAGGAGC  
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC  
GCGAGCTGTATTGATGCAAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTTC  
TGGTTATATCTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT  
GAGATAGGGAGAG

## **FIGURE 9**

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG  
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCACACCAATGCCGGGCACCTAC  
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT  
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTGGTCTTAAGGCAGGTTT  
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGAC  
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA  
GGACCGGGATGCCCTGCGCCTCACCCCTGGAGCAGATTGACCTCATACGCCGCATGTGTGCCT  
CCTATTCTGAGCTGGAGCTTTGTACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC  
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT  
CTACATGTCTGGAGTGGCTACCTGACGCTCACCCACACCTGCAACACACCCCTGGGCAGAGA  
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG  
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC  
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCC  
GGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC  
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGC AACCCATCAGCCAATGT  
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCTATTGGATCCAAGTTCATCGGGA  
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATAC  
CCGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT  
TCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC  
AAAGCCCCCTTGAGAGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCTTGCCACTCCGACCTC  
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA  
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG  
TCCTTGCAAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC  
TGCCAGATGTCACTGTAGCAAGCCACAGACCCCCACAAAGTTCCCTGTTGTGCAGGCACA  
AATATTTCTGAAATAAATGTTTTGGACATAG

## **FIGURE 10**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYPASTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG  
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND  
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRVLTLTHTCNTPWAESSAKGVHSFYNNISGL  
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVVSQAPVIFSHSAARGVCNSARNVPDDILQ  
LLKKNGGVVMVLSMGV IQCNPSANVSTVADHFDHIKAVIGSKFIGIGDYGAGKFPQGLE  
DVSTYPVLIEELLSRGWSEEEELQGVLRGNLLRVFRQVEKVEENKWQSPLEDKFPDEQLSSS  
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

### **N-glycosylation sites.**

amino acids 58-62, 123-127, 182-186, 273-277

### **N-myristoylation sites.**

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

### **Renal dipeptidase active site.**

amino acids 134-157

## FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGGGATCCGCGGCCG  
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCAGCA  
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATCGGGACTTCCGCTCGTGACGCGCCAC  
AACGACCTGCCCTTGGTCTTAAGGCAGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG  
CAATTTACAGTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT  
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG  
CAGATTGACCTCATACGCCGATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC  
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC  
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC  
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA  
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA  
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGCGGGCCCTGGAAGTGTACAG  
GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGGTGTGTGCAACAGTGTCTCGAATGTTCC  
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCTGTGAGTGTCTTTGTCCATGG  
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTGACACCACATC  
AAGGCTGTCTATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT  
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTGTGAGTCTGTG  
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTTCGTGGAACCTGCTGCGGTCTTCAGACAA  
GTGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCCTTGAGGACAAAGTTCCTCGGATGA  
GCAGCTGAGCAGTTCTTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT  
CAGGCCAGGAACCTCACTGAGATTCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA  
GTCTCAGAGTCTTCCCCCACCCTGACAAAACCTACACATGCCCCACCGTGGCCAGCACCTGA  
ACTCTGGGGGACCGTCACTCTCTCTTCCCCCAAACCAAGGACACC

## **FIGURE 12**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSPANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVPRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
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[illegible][illegible]

## **FIGURE 14**

><ss.DNA38113  
><subunit 1 of 1, 422 aa, 1 stop  
><MW: 46302, pI: 9.42, NX(S/T): 6  
MPAGRRGPAAQSARRPPPLPLLLLLCVLGAPRAGSGAHTAVIS PQDPTLLIGSSLLATCSV  
HGDPPGATAEGLYWTLNGRRLLPPELSRVLNASTLALALANLNGSRQSGDNLVCHARDGSIL  
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYS LKYKLRWYGQDNTCEE  
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVS RVGG  
LEDQLSVRWVSP PALKDFLFQAKYQIRYRVEDSV DWKVVDVSNQTSCRLAGLKPGTVYFVQ  
VRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPFVRRELKQFLG  
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGRTARGPAR

### **Signal sequence.**

amino acids 1-30

### **Transmembrane domain.**

amino acids 44-61

### **N-glycosylation sites.**

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 413-417

### **N-myristoylation sites.**

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,  
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

### **Amidation site.**

amino acids 3-7, 79-83, 411-415

### **Growth factor and cytokines receptors family signature 2.**

amino acids 325-331



## **FIGURE 16**

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDSCSNREDIYSSAKVKVKAIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC  
SSKFAAVGFGHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

### **Signal sequence.**

amino acids 1-19

### **Transmembrane domain.**

amino acids 170-187

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 30-34, 283-287

### **N-myristoylation sites.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGAGCCGGCAGGGAGCGAACCAGGACTG  
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAAGCGCGGGGGCTGGAGCACCACCAA  
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT  
GCGAGAGGACCCCGGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTGTC  
TGCTCCTGGGCCTGGCGGCCGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC  
CCGGGACACCCCGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG  
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGCTCCGGGAGAGAAAGCGAGGGCGGGA  
GGCCGGGACTGCCGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGCGGGACCCGCGGGG  
CCCAACGGGCCTGCCGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC  
CGAGAGCCGGGTGCCCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCGCGTGTGGTGAACG  
AGCAGGGACATTACGACGCCGTCAACGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC  
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA  
ATCCATTGCCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGG  
GGCCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC  
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTCTGGTGTACTCCGA  
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAAGTGAGCTCATGCTCTCACTCC  
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCTGGAATATT  
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTCTGCTGCTGGCAAGGAATGGGAAC  
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCCAAGACCA  
GAGGAGTGTGCTGTGCTGGCAAGTGTAAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT  
GGGGTGTCTCTTCTGTGCTCTGCTTCTCTGGATCTCCCCACCCCTCTGCTCCTGGG  
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP  
GEKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSASFSAKRSESRVPPPSDAPLP  
FDRVLVNEQGHYDAVTGKFTCQVPGVYFVAVHATVYRASLQFDLVKNGESIASFFQFFGGWP  
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

### **Signal sequence.**

amino acids 1-15

### **N-myristoylation sites.**

amino acids 11-17, 68-74, 216-222

### **Cell attachment sequence.**

amino acids 77-80

## FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG  
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCAACAGACCCAT  
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG  
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC  
CTGAACAGGAAGGAGAGTTTCTGTCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA  
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG  
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG  
CAAGTGGGCTGGAACATGCAGCTGCTGCCCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG  
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGTGTGCTCGCAACGCCA  
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC  
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCAA  
CTGGGAGGTCAACGGGAAGACAATCATCCCCATAAGAAGGGTGCCCTGGTGTTCGCTCTGCA  
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCC  
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGCTCTCAACATCAGCACCTGCCACTG  
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC  
ACGGCCGGTTCGGGAGGAGGAGTGTCTGTCGTCTGTGACATCGGCTACGGGGAGCCACG  
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT  
CATGGTGTCTTCAGAGGCAGACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAAGGCG  
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGACGGACATCCTCGCCTTCTATCTGGGCCGC  
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGGCT  
CACCTACAAGACCGCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA  
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT  
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC  
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCCAGGGTCCT  
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACC GGCTCTGCTTACCTGTCTGC  
CCACCTGTCTGGAACAAGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA  
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG  
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA  
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCAGAC  
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG  
CTGAAAAAAAAAAAAA

## **FIGURE 20**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV  
QPPAADMRRILDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV  
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCGAGQTAIEAFVCAYSPPG  
NWEVNGKTIIPYKKGAWSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQNHGRLNISTCH  
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC  
FMVSSEADTYRARMKCQRKGGVLAQIKSQKQVDILAFYLGRLTETNEVTDSDFETRNFWIG  
LTYKTAKDSFRWATGEHQFTSFAFGQPDNHGLVWLAAAMGFNCVELQASAAFNWQDQRCK  
TRNRYICQFAQEHISRWGPGS

**Signal sequence.**

amino acids 1-26

**Transmembrane domain.**

amino acids 110-124

**N-glycosylation sites.**

amino acids 144-148, 243-247

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 45-49

**N-myristoylation sites.**

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,  
288-294, 331-337, 398-404

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 204-215

**EGF-like domain cysteine pattern signature.**

amino acids 249-261, 280-292

**C-type lectin domain signature.**

amino acids 417-442

CSDEP03001

## FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCGGGTCCCCGAGCGTCCCGCGCCCT  
CGCCCCGCGC**ATG**CTCCTGCTGTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTGC  
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCCGAGGCAAG  
TCAGACTGTTGTCAGAGGCTGAAAAACCAACCTTTGATGACAGAATTTCTCAGTGAAGTCTTACC  
ATCATTTCCCGTTATGCCCTTCACTACGGTTTCTTGCAGAATGCTGAACAGAGCTTCTGAAGA  
CCAGGACATTGAGTTCAGATGCAGATTCCAGCTGCAGCTTTATCCCAACTTCACTATGC  
TTATTGGAGACAAAGTGTATCAGGGCCGAAATTACAGAGAGAGAAAAAGAGAGTGGTGATAGG  
GTAAAAGAGAAAAGGAATAAAACCAAGAAGAAATGGAGAGAAGGGGACTGAAATATTTCAG  
AGCTTCTGCAGTGATTCCAGCAAGGACAAAGCCGCTTTTTCTGAGTTATGAGGAGCTTC  
TGCAGAGGCGCTGGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCCCAGCAGCTGTCCGGG  
AGGCTGAGCGTGGACGTGAATATCTTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC  
GCTTCACAACAGCAGGCAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCTCCCCCAT  
CTACTGTCAATTAACCAAAATGAAACATTTGCCAACATAATTTTTAAACCTACTGTAGTACAA  
CAAGCCAGGATTTGCCAGAAATGGAATTTTGGGAGACTTTATCAITAGATATGACGTCAATAG  
AGAACAGAGCATTTGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA  
AAGACCTTCTCCTTTACCCAAGAAATGTGGTATTCTGTCTTGACAGCAGTGCTTCTATGGTG  
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCAACAATTTCTCATGACCTCCGACCCCA  
GGACCGTTTCAGTATCATTTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCCTTGATAT  
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGACATTCACCATATGTCACCCACTGGA  
GGCAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA  
CGTGGCATTTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTTCTGACGGATGGGAAGCCACGG  
TCGGGGAGAGCGCACCCCTCAAGATCCTCAACAACCCGAGAGGCGCCCGAGGCGCAAGCT  
TGCACTCTTCAACATTTGGCATCGGCAACGACGTGGACTTCAGGCTGTCTGGAGAAACTGTCTGT  
GGAGAACTGTGGCTCACACGGGCGGTGCACGAGGAGGAGGACGAGGCTCGCAGCTCATCG  
GGTCTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGATCGATTATCCCCCAGC  
TCAGTGGTGCAGGCCACCAAGACCCCTGTTCCCCAACTACTTCAACGGCTCGGAGATCATCAT  
TGCGGGGAAGCTGTGGACAGGAAGCTGGATCACTTGCAGTGGAGGTCAACGCCAGCAACA  
GTAAAGAAATTCATCATCTGAAAGACAGATGTGCCTGTGCGGCCCTCAGAAGGCAGGGAAGAT  
GTCAAGGAAGCCCGGCTTGGAGGCGATGGAGAGGGGGACCAACCAATCGAGCGTCT  
CTGGAGTCACTCACCAAAAGGAGCTGTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG  
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCTCACTCCC  
TTCACTTCCATGAAGCTGAGGGGGCCGCTCCACGCATGGATGGCTGGAGGAGGCCACGG  
CATGTGCGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGGTGGCACGCAGC  
CAGGACCTTTGCTCAAGAAGCCAACTCCGTCAAAAAAACAACCAACCAAAAAAAGA  
CATGGAGAGATGGTGTTTTCTCTCCACCACTGGGATACGAT**GGA**GAAGATGGCCACT  
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGTGGCACCTTGATCTTGGACCTC  
CCAGCTTCAGAACTGTGAGAAATAAATGTGTGTTTAAAGCTAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQLRLLTKPLMTFSVKSTIIIS  
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE  
KRNKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS  
VDVNILESAGIASLEVLP LHNSRQRGSGRGEDDSGPPPTVINQNETFANIIFKPTVVQQAR  
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASVMGK  
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVKWDHLISVTPDSIRDGVYIHHMSPTGGTD  
INGALQRAIRLLNKKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAAARGQVCIF  
TIGIGNDVDFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV  
QATKTLFPNYFNGSEII IAGKLVDRKLDHLHVEVTASNSKKFII LKTDVVPVRPQKAGKDTV  
SPRPGDGEGEDTNHIERLWSYLTTELSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS  
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLLKKPNSVKKKQNKTKKRHR  
DGVFPLHHLGIR

### **Signal sequence.**

amino acids 1-14

### **N-glycosylation sites.**

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

### **Glycosaminoglycan attachment sites.**

amino acids 213-217, 391-395

### **N-myristoylation sites.**

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

## FIGURE 23

CGGACGCGTGGGGTGCCCGAC**ATG**GCGAGTGTAGTGCTGCCGAGCGGATCCAGTGTGCGGC  
GGCAGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCGCGG  
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA  
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACGCTACTGAA  
TCCCAACAGGCAGACATTATTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT  
TGCTGAATTTTCTAGCAGTGAACTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA  
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT  
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG  
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA  
GGGAACACAGAGCTAAAAGGCAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC  
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG  
AGCACCCCTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT  
CAAGTGCACATTAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA  
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG  
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTCAATCAATAACCTAAACAAA  
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAGCTCACTCGGATTA  
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCTCCCAACAACACCACCACCA  
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCTGAGCAGGTGAAGAAGGC  
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT  
GCTGTGCTTGCTCATATTCTGGGCGCTATTTTGCCAGACATAAAGGTACATACCTCACTC  
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA  
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCT**AGAT**CAGCCTTTTGTGTTCAAT  
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

## **FIGURE 24**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518  
<subunit 1 of 1, 440 aa, 1 stop  
<MW: 48240, pI: 4.93, NX(S/T): 7  
MASVVLPSGSQCAAAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC  
QVNKSDDSVIQLLNPQRQTIYFRDFRPLKDSRFQLLNFSSELKVS LTNVSI SDEGRYFCQL  
YTDP PQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTLKG  
KSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPKQVHIQMT  
YPLQGLTREGDALELTCEAIGKPQPMVMTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR  
CEASNIVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH  
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE  
KKEYFI

### **Signal sequence.**

amino acids 1-36

### **Transmembrane domain.**

amino acids 372-393

### **N-glycosylation sites.**

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,  
430-434

### **Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

### **N-myristoylation sites.**

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,  
411-417, 427-433, 428-432

[illegible]

GGGCGGGTGGACGCGGACTCGAACCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCGGA  
CCGCGCCAGGAAGACTGAGAGCGCGGCTCTGCCCGCCGGCTCTCCTGCGCGCCGCGCGGCTC  
CCGGGACAGAAGTGTGCTCCAGGCTCCCTGTGCTGCTGCCGTCTCTGCTACTGGCCCT  
GGGGCCTGGGGTGCAGGGTGCCCATCCGGCTGCAGTGCAGCCAGCCACAGACAGTCTTCT  
GCATCTGCCCGCGAGGGGACACGGTGCCTCCGAGACGTGCCACCCGACCGGTGGGGCTGTAC  
GCTCTTTGAGAACGGCATCACCATTGCTCGACGCAAGCAGCTTTGCGCGCTGCTCGCGGCTGGA  
GCTCTGCAGCTGTGCACAAACAGATCGCAGCTGCGCCTGCCCTGCCCGCTGCTGCTGTGG  
ACCTCAGCCACAACAGCCTCTGGCCCTGGAGCCCGGCATCTGGACACTGCCAACGTGGA  
GCGTTCGCGCTGGCTGCTGTGTTGGGCTGCAGCAGTGGACAGAGGGCTCTTCAGCCGCTTGTGG  
CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG  
GCTCCGGGGCCTGACGCGCTTCGCGCTGGCCGGCAACACCGCATTTGCCAGCTGCGGCC  
GAGGACCTGGCCGGCTGGCTGCCCTTCAGCCAGCTGGATGTGAGCAACCTAAGCCTGCAGGC  
CCTGCTTGGCGACCTCTCGGGCTCTTCCCGCGCTCGCGCTGCTGGCAGCTGCCCGCAACC  
CCTTCAACTGCGTGTGCCCTTGAGCTGGTTTGGCCCTGGGTGGCGAGAGCCACGTGACA  
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT  
GGAGCTTGATACGCCGACTTTGGCTGCCCAGCACACACACACAGCCACAGTGCACCA  
CGAGGCCCGTGTGGTGGGAGCCCAACGCTTGTCTTCTAGCTTGGCTCTACTGGCTTAGC  
CCACAGCGCGCGGCTGACTGAGGCCCGGCGCGCTTCCATGCCCCACGCACTGTAGGGCC  
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCCTCAATGGGGGCATGCCACCTGG  
GGACACGGCACCCACTGGCGTGTGTGTGCCCCGAAGGCTTCAGGGCTGTATGTGTAGAGC  
CAGATGGGGCAGGGGACAACGCGCCAGCCTTACACAGTCAACGCGAGGCCACACGCTCCCT  
GACCTTGGGCATCGAGCGCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC  
AGGGAGGCTCCGTGCAGCTCAGGAGCCTCCGCTTCACTATCGCAACCTATCGGGCCCTGAT  
AAGCGCTGTGTAGCTGCGACTGCTGCTGCTCGCTCGTGTAGTACACGCTACCCGAGTGGC  
GCCCAACGCCACTTACTTCGCTGTGTGTCATGCTTTGGGGCCGGGCGGGTGCAGGAGCG  
AGGAGAGCTTGGGGGAGGCCATACACCCCGACCGTCCACTCAACACAGCGCCAGTCAAC  
CAGGCCCGCGAGGGCAACTCGCCCTCTCTATTGCGCCCGCTGGCCCGGGTGGCTCCTGGC  
CGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGGGGGCGGGCATGCCAGCAGCGG  
CTCAGGACAAAGGGCAGGTGGGGCCAGGGCTGGGCCCTGGAACGTGAGGGAGTGAAGGT  
CCCTTGGAGCCAGGCGCAGGCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA  
GCTGTAGGTGCCACTATGAGGCTTCCAGGCGCTGGCTCGAGTCAACCTCCACGCAAGC  
CTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCAGTGTGAGATGGC  
CAGCCCCCTCTGCTGCCACACCAAGTAAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA  
CAGGGCTGTGTGACCAACAGCTGGGCCCTGTTCCCTCTGGACCTCGGCTCTCTCATCTGTGAG  
ATGCTGTGTGGCCAGCTGACGAGCCTTAAGCTCCCGAACCGAGTGGCTATGAGACAGTGT  
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC  
GCATGCTTGGGCCCTGCTGGGCTCTCCCACTCAGGGCGGACCTGGGGGGCCAGTGAAGGAAG  
CTCCGCGAAAGACAGAGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG  
AAGCGAAGGAAACAAAGAACTGGAAGGAAGATGCTTTAGAAACATGTTTGTCTTTTAA  
AATATATATATATTTATAAGAGATCCTTTCCCATTTATCTGGGAAGATGTTTTTCAAATC  
AGAGACAAGGACTTTGGTTTTTGTAAACAAACGATGATATGAAGGCTTTTGTAAAGAAAA  
ATAAAAAAAAAA

## FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLLLLLLALGPGVQGPCSGCQCSQPQTTFCTARQGTTPRDPVPPDVTGLYVFEN  
GITMLDASSFAGLPGLQLLDLSQNQIASLRRLPRLLLDLSHNSLLALEPGILDANVEALRL  
AGLGLQLLDEGLFSRLRNLDVSDNQLERVFPVIRGLRGLTRLRLAGNTRIAQLRPEDLA  
GLAALQQLDVSNSLSLQALPGDLSGLFPRLRLAAARNPFCVCLSWFGPWVRESHVTLASP  
EETRCHFPKPNAGRLLLELDYADFGCPATTTTATVPTRPVVREPTALSSSLAPTWLSPTAP  
ATEAPSPPTAPPTVGPVPQPDCCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQ  
GTRPSPPTVTPRPPRSLTLGIEPVSPSTSLRVGLQRYLQGSVQLRSLRLTYRNLSGPDKRLV  
TLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE  
GNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGVGPGAGPLELEGVKVPLEP  
GPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

### Signal sequence.

amino acids 1-23

### Transmembrane domain.

amino acids 501-522

### N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

### Tyrosine kinase phosphorylation site.

amino acids 262-270

### N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

### EGF-like domain cysteine pattern signature.

amino acids 355-367

### Leucine zipper pattern.

amino acids 122-144, 194-216

## FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCCTTACCCGCCCCGCCACC  
TCCTTGCTACCCCACTCTTGAAACCAACAGCTGTTGGCAGGGTCCCCAGCTC**ATG**CCAGCCTC  
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCCACTCAGAGAGC  
CGGCACTCTCAGTTGCCCTCTGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTCGC  
ATGGCTCTGCTGACCCAAACAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA  
GGGGACAGGAGGCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCCGGAGCAGA  
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC  
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCCATTAACGCCACCTCCAA  
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC  
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC  
CTGTTTCAAGACGTGACTTTCACCATGGGTGAGTGGTGTCTCGAGAAGGCCAAGGAAGCA  
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCCACCCGGACCGGGCTACAACAGCT  
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCATAAATCCCCGG  
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAACTG**TGATT**  
GTGTTATAAAAAGTGGCTCCAGCTTGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA  
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC  
CCGTTCTCTCACTTTTCCCTTTTCATTCCACCCCTAGACTTTGATTTTACGGATATCTTG  
CTTCTGTTCCCATGGAGCTCCG

## **FIGURE 28**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFL LAPKGGPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTEQLSLRREV  
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLPIN  
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG  
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVII PRARAKLNLSPHGTF LGFVKL

### **Signal sequence.**

amino acids 1-40

### **N-glycosylation site.**

amino acids 124-128

### **Tyrosine kinase phosphorylation site.**

amino acids 156-164

### **N-myristoylation site.**

amino acids 36-42, 40-46, 179-185, 242-248

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 34-45

## FIGURE 29

CACTTTCTCCCTCTCTTCTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCGAGAGAC  
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA  
CGCGCCCCCACCTTCTCTTCTGCACTGCGGTCTCCGGAAGACCTTTCCCTCGTCTCTGTT  
TCCTTACCAGAGTCTGTGCATCGCCCCGGACCTGGCGGGAGGAGGCTTGGCCGGCGGGAGA  
TGCTCTAGGGGGCGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCGGCAGGAAGATGGGC  
TCCGCTGGACAGGACTCTTGCTGGCGTACTGCTGCTCTTTCCTTTGGCTTCTGGCCTGGT  
CCTGAGTCGTGTGCCCCATGTCAGGGGGAACAGCAGGAGTGAGGGGAGCTGAGAGGCTGCG  
CGTGCCTCCGGACCATGCGGAGAGGCTGAAGAAACAATGAAAAATACAGGCCAGTCAAG  
GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCGCTGCTGTGACCCCGGTACCTCCATGTACCC  
GGCGACCGCGGTGCCCGAGATCAACATCACTATCTTGAAGGGGAGAAGGGTGACCGCGGAG  
ATCGAGGCTCCAAGGGAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACATGGA  
CCCAAAGGGCAGAAGGGCTCCATGGGGGGCCCTGGGGAGCGGTGCAAGAGCCAGTACGCCCG  
CTTTTCGGTGGGCCGGAAGAAGCCCATGCAAGCAACCACTACTACAGACGGTGATCTTCG  
ACACGGAGTTTCGTGAACCTCTACGACCACTTCAACATGTTTACCGGCAAGTTCTACTGTCTAC  
GTGCCGGCTCTACTTCTTTCAGCCTCAACGTGCACACCTGGAACCAAGAAGGAGACTTACT  
GCACATCATGAAGAACGAGGAGGAGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA  
TCATGCAAAGCCAGACGCTGATGCTGGAGCTGCGAGAGCAGGACCAAGTGTGGGTACGGCTC  
TACAAGGGCGAACGTGAGAACGCCATCTTACGAGGAGGCTGGACACCTACATCACTTTCAG  
TGGTACTGTGTCAGACCGCCACCGAGCCCTAGCTGGCGGGCCACTCTCTTCTCTGCGC  
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCCTGGACTCCGACTC  
CCTGGCTTTGGCATTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC  
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATACCAGGGGGGGGCACCCGC  
GAGAACCCTCTGGACCTTTCGCGGCCCTCTTGCACACATCTCAAGTGACCCCGCACGGC  
GAGACCGGGTGGCGGCAGGGCGTCCAGGGTGCGGCACCGCGCTCCAGTCTTGGAAATA  
ATTAGGCAAAATCTAAAGGTCTCAAAGGAGCAAAAGTAAACCGTGGAGGACAAAGAAAAGGG  
TTGTTATTTTGTCTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCTTTTCAGTTGAG  
ACTCTGCTTAAGAGAAGATCCAAGTTAAAGCTCTGGGTGAGGGAGGGGCCGGGGCAGG  
AAACTACCTCTGGCTTAATCTTCTTAAGCCACGTAGGAACCTTTCTTGAGGATAGGTGGACC  
CTGACATCCCTGTGGCCTTGCCCAAGGGCTCTGCTGGTCTTTCTGAGTCACAGCTGCGAGGT  
GATGGGGCTGGGGCCCGAGGCGTCAGCCTCCAGAGGGACAGTCAGCCCTGCTTTGGC  
TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCTGACAGTGCCAGGGACCCCTGGGTCCCCCA  
GGCTTGAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC  
ACCCCTGTGCTTCCAGAGCCCTGGGGGGTGGTCCCATGCTGCCACCTGGCATCCGCT  
TTCTGTGCCCTCCACACAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT  
TATAAAACACCTCAAGAGCACTGCAGTCTCCATCTCTCTGTTGGGTAAAGCATACCGCTT  
CCAGCTGTGTTGTGTTGGTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCACTGCGCTT  
CATCCAGGCTCTGACCACTAGCCTGAGAGGGCTTTTCTAGGCTTTCAGAGCAGGGGAGAG  
CTGGAAGGGCTAGAAAGCTCCCGCTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTG  
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTGAGGATTCACCTCTCAGGAGC  
TGGGTGCGAGGAGGCAATAGCCCTGTGGCAATTGCAGGACAGCTGGAGCAGGGTTGCG  
GTGCTCTCCAGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC  
ATAGCCCTCTCTCACTCACCCCATGTTGATGCCAGGGTCACTCTGTGCTACCCGCTGGGCC  
CCCAAAACCCGCTGCTCTTCTTCCCCCATCCCCCACTGGTTTGAATCAATCTGC  
TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT  
CTGCGGGTCAAGCTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACTC  
GCTGCTTAAGCTCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

## **FIGURE 30**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MSRSGQGILLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELSPDPHAERAEBQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVI FDTFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGD RSIMQSSLMLELREQDVVW
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

### **Signal sequence.**

amino acids 1-25

### **N-glycosylation site.**

amino acids 93-97

### **N-myristoylation sites.**

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

### **Amidation site.**

amino acids 150-154

### **Cell attachment sequence.**

amino acids 104-107

## FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTCGCCGAGACCCCGCGCGGATTGCGCGGTCTTCCCGCGG  
 GCGCGACAGAGCTCTCTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCTCGACGCCA  
 GAGAGAAATCTCATATCTGTGCAGCCTTCTTAAAGCAAATTAAGACCAAGGGAGGATTAT  
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTTCGGGGGAGAAGGAG  
 CTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGTAGTCAGAATT  
 GCCTCAAAAAGAGTCTAGAAGATGTTGTGCTTACATCCAGTCATCTCTTCTAAGGGAATC  
 AGAGGCAATGAGCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTTGCTGTTCAAC  
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA  
 GACAACCCAACCTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACAGCA  
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG  
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAAGCAGTCACCTCCC  
 TAGCCCATCATCACACAGATTATTCAAGGCCACCGATATCTCATGGAGAGACACTTTCT  
 CAGAAGTTTGGATCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA  
 GCTCCTTGCTTATAAGGAAAAAGGCCATTTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA  
 TAGCTCATCTGCTGCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA  
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTTCTACCCACCAATGCTTCAGTGACACC  
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC  
 AGCCTCCCACGACCTCATTTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG  
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGAATCGAAAGGCAGCTTAGA  
 AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCTTA  
 CTGCATTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT  
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCCAGAAAAATCAGTACGGCCTTCC  
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTTGGTGATAGGCC  
 TCGTCTCTCGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT  
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT  
 TAGTAACCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG  
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTTCTCTTTTTTTTTTTGGAGACAGAGTCTT  
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC  
 CTGGGTTCAAGCGATTCTCTGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA  
 CCACACCTGGGTGATTTTGTATTTTTAGTAGAGACGGGGTTTACCAGTGTGGTCAGGCTG  
 GTCTCAAACCTCTGACCTAGTGATCCACCCCTCTCGGCTCCCAAAGTGCTGGGATTACAGG  
 CATGAGCCACCACAGCTGCCCCCTTCTGTTTATGTTTGGTTTGTGAGAAGGAATGAAGTG  
 GGAACCAATTAGGTAATTTGGGTAATCTGTCTCTAAAAATATTAGCTAAAAACAAGCTCT  
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCACCTGGCTTTTATGCAAAA  
 GAAACAGGTTAGGACATCTAGGTTCCAATTCAATCACATTCTTGGTTCAGATAAAATCAAC  
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTTTAAAACTTATT  
 CCAGATGTAGTTCTTCCAATTAATATTTGAATAAACTCTTTGTACTCAA

## **FIGURE 32**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGEGSLTYTLVIIICPLTLRLSASQNCLKKSLEDVVIDIQSSLSKGI RGN E P V Y T S T Q E D
C I N S C C S T K N I S G D K A C N L M I F D T R K T A R Q P N C Y L F F C P N E E A C P L K P A K G L M S Y R I I T D F P
S L T R N L P S Q E L P Q E D S L L H G Q F S Q A V T P L A H H H T D Y S K P T D I S W R D T L S Q K F G S S D H L E K L F
K M D E A S A Q L L A Y K E K G H S Q S S Q F S S D Q E I A H L L P E N V S A L P A T V A V A S P H T T S A T P K P A T L L
P T N A S V T P S G T S Q P Q L A T T A P P V T T V T S Q P P T T L I S T V F T R A A A T L Q A M A T T A V L T T T F Q A P
T D S K G S L E T I P F T E I S N L T L N T G N V Y N P T A L S M S N V E S S T M N K T A S W E G R E A S P G S S Q G S V
P E N Q Y G L P F E K W L L I G S L L F G V L F L V I G L V L L G R I L S E S L R R K R Y S R L D Y L I N G I Y V D I
```

### **Signal sequence.**

amino acids 1-25

### **Transmembrane domain.**

amino acids 384-405

### **N-glycosylation sites.**

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 415-419

### **Tyrosine kinase phosphorylation site.**

amino acids 50-57

### **N-myristoylation sites.**

amino acids 4-10, 48-54, 315-321

## FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC  
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT  
GTCCAGTGTGCTTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC  
CCAAAAGGCAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA  
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG  
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA  
ATGTGACAGCAACACGATGTTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG  
TTTATTTCAGAGTGTCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC  
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA  
TGAAATTCAGGTCTAGCTGGGTATTTATTCAGCAAAAAGGCTTGGAACCTCCCTTCCGAAATT  
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAAACAACAGATATTTGGCTGGCCTGCAGA  
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACACTGCAGGGTCCCTGAGTAAAT  
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA  
GCCCATATTTGATGAGTATTTTGGGTTGTTGTAAACCAATGAACATTGCTAGTTGTATCA  
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA  
AACTAAAATGAATGGAAATTCCTAAAAA

## FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777  
><subunit 1 of 1, 235 aa, 1 stop  
><MW: 25982, pI: 9.09, NX(S/T): 2  
MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK  
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT  
RCFDMEYEGDNSGPMTKFIQSAAPKSLLFMVITYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS  
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

### Signal sequence.

amino acids 1-20

### N-glycosylation sites.

amino acids 120-124, 208-212

### Glycosaminoglycan attachment site.

amino acids 80-84

### N-myristoylation sites.

amino acids 81-87, 108-114, 119-125